Scotland's Rural College

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Assessing the Spatial Distribution of *Ixodes ricinus* in Scotland Using a Bayesian Approach

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Introduction

In Northern and Western Europe *Ixodes ricinus* tick is a vector of several pathogens, including the complex of *Borrelia* bacteria that causes Lyme disease [1], whose reported incidence is increasing in Scotland [2]. Predictive maps with the spatial and seasonal distribution of vectors are important tools in assessing the risk of vector-borne diseases, enabling better targeting of surveillance and control, as well as increasing awareness [3].

The objectives of this study are to identify the climate, habitat, topography and host related predictors of *I. ricinus* abundance and to create a risk map of ticks across mainland Scotland.

Methods

- ✓ Questing nymphs were counted by scientists during tick abundance surveys (2006 - 2017).
- ✓ An average of 15 survey transects were performed in each site and visit.
- ✓ To account for the complex structure of the dataset a Bayesian model [4] was fitted with a zero inflated Poisson distribution and two random effects (site and number of drags per site).
- ✓ The model fixed effects were georeferenced environmental variables.
- ✓ The model was assessed using Bayesian information criteria and cross validation leave-one-out.
- ✓ The model and the risk map were developed using R software.

Fig. 1: Tick transects involve dragging vegetation with a 1*1m blanket for 10 meters.

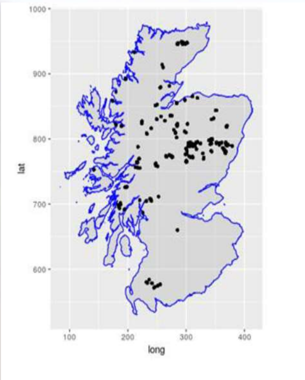

Fig. 2: Location of tick survey sites.

Results

Model expression: Count of nymphs ~ climate + habitat + hosts + month (April slope) + f (site) + f (drag)

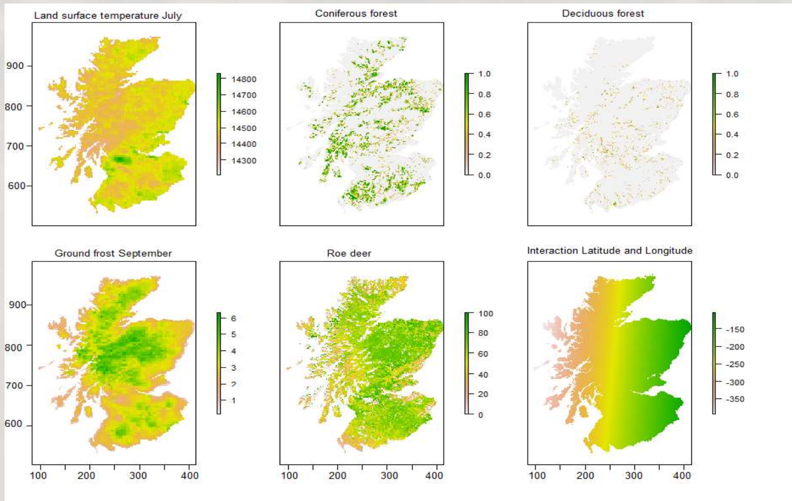

Fig. 3: Plot showing the distribution of the significant predictors of nymph abundance: land surface temperature in July; proportion of land cover that is coniferous woodland; proportion of land cover that is deciduous woodland; ground frost in September and roe deer presence. Interaction between latitude and longitude was included in the model although was not significant.

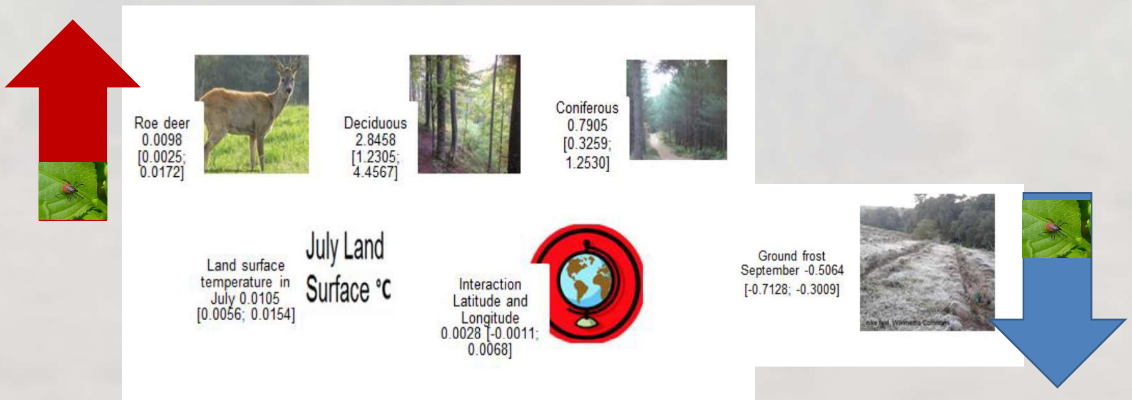

Fig. 4: The predictors that have a positive influence on nymph abundance (red arrow) are roe deer presence, deciduous and coniferous forest and land surface temperature in July. Ground frost in September has a negative effect (blue arrow) on nymph abundance.

The strength and the direction of the effect of each variable are given by the value of the posterior mean (see model's coefficients and respective 2.5% and 97.5% quartiles in brackets). Month of tick sampling was then included in the model and it improved the model's fit.

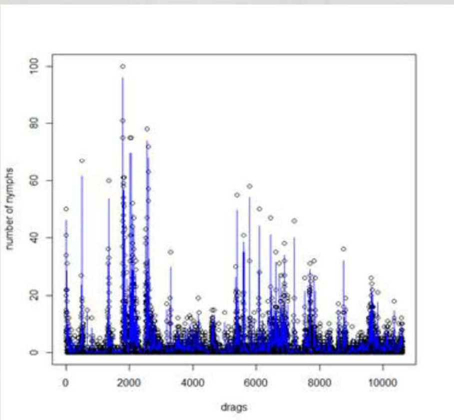

Fig.5: Graph showing the model's goodness of fit (the predicted values (blue lines) are very close to the observed ones (black dots)).

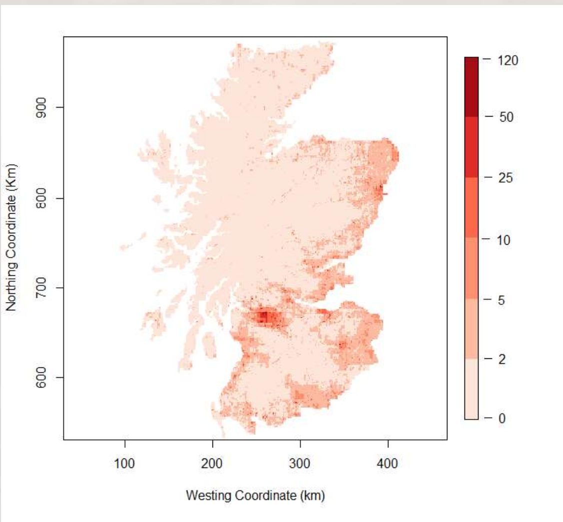

Fig. 6: Risk map of predicted nymph abundance (in April, which is the month of highest questing nymph abundance).

Discussion and conclusions

- ✓ The count of nymphs per drag was chosen as the response variable because nymphs have the highest risk of biting and transmitting the bacteria that causes Lyme disease in humans.
- ✓ The selected model shows significant and positive relationships between tick abundance and temperature in July, roe deer presence, coniferous and deciduous forest, and a negative association with frost in September.
- ✓ The model choice seemed suitable to capture data complexity (the model fits the data well) and the significant predictors (climate, deer and habitat) are supported by knowledge from the published literature.
- ✓ The predictive risk map is likely to be most robust for the Grampian region, where most data were collected, and less accurate for areas where there were few data from surveys, such as the West coast of Scotland. This is useful in highlighting where data collection efforts are now needed for more accurate models.

Bibliographic references: [1] - Medlock, J. M. et al. Driving forces for changes in geographical distribution of *Ixodes ricinus* ticks in Europe. Parasit. Vectors **6,** 1–11 (2013); [2] - Mavin, S., Watson, E. J. & Evans, R. Distribution and presentation of Lyme borreliosis in Scotland-analysis of data from a national testing laboratory. J. R. Coll. Physicians Edinb. **45,** 196–200 (2015); [3] - Elith, J. & Leathwick, J. R. Species Distribution Models: Ecological Explanation and Prediction Across Space and Time. Annu. Rev. Ecol. Evol. Syst. **40,** 677–697 (2009). [4] - H. Rue, S. Martino, and N. Chopin. Approximate Bayesian inference for latent Gaussian models using integrated nested Laplace approximations (with discussion). Journal of the Royal Statistical Society, Series B,71 (2):319{392, 2009.

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